



# results of BLAST

## BLASTP 2.2.10 [Oct-19-2004]

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1105739873-2607-128700542711.BLASTQ4

### Query=

(101 letters)

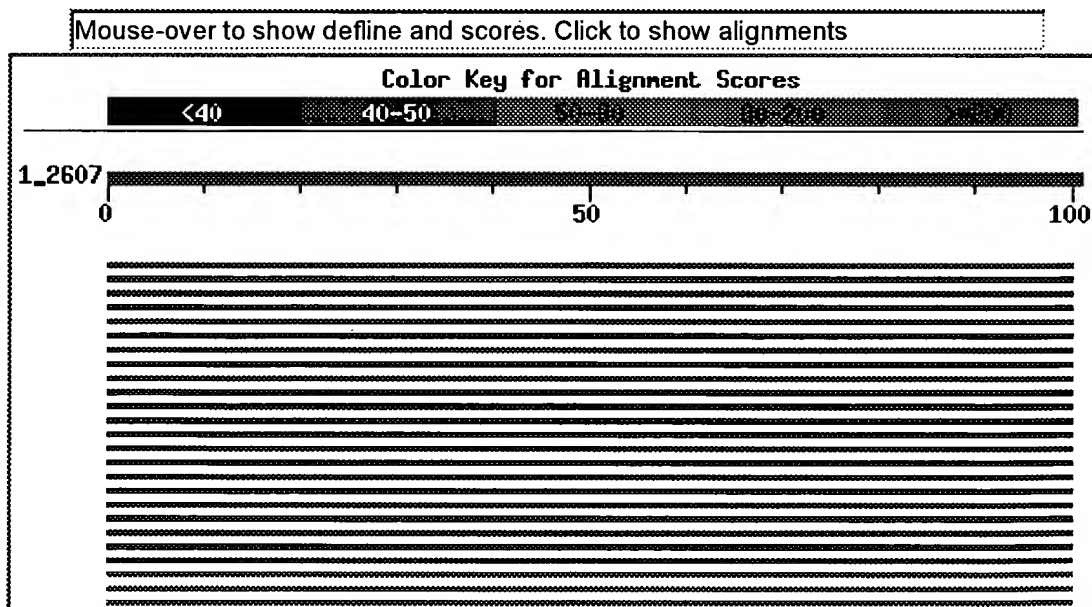
### Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples  
2,306,668 sequences; 784,723,489 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

### Taxonomy reports

## Distribution of 700 Blast Hits on the Query Sequence



### Related Structures

Sequences producing significant alignments:

| Score  | E     |
|--------|-------|
| (bits) | Value |
|        |       |

|                                  |   |     |       |   |
|----------------------------------|---|-----|-------|---|
| gi 15706263 emb CAC69989.1       | bromodomain containing 2 [Homo ...      | 217 | 6e-56 | G |
| gi 4826806 ref NP_005095.1       | bromodomain containing protein ...      | 217 | 6e-56 | G |
| gi 1082363 pir A56619            | female sterile homeotic (fsh) homolo... | 217 | 6e-56 | G |
| gi 51770504 ref XP_489783.1      | similar to MMRING3.1.2 [Mus mu...       | 217 | 6e-56 | G |
| gi 57094404 ref XP_532103.1      | PREDICTED: similar to Bromodom...       | 217 | 6e-56 |   |
| gi 47059183 ref NP_997660.1      | bromodomain-containing 2 [Ratt...       | 217 | 6e-56 | G |
| gi 6753910 ref NP_034368.1       | bromodomain containing 2 [Mus m...      | 217 | 6e-56 | G |
| gi 55956582 emb CAI11405.1       | bromodomain-containing protein ...      | 217 | 6e-56 |   |
| gi 55725298 emb CAH89514.1       | hypothetical protein [Pongo pyg...      | 217 | 6e-56 |   |
| gi 52545923 emb CAH56179.1       | hypothetical protein [Homo sapi...      | 217 | 6e-56 |   |
| gi 12802525 gb AAK07919.1        | ring 3 [Mus musculus]                   | 217 | 6e-56 | G |
| gi 1370115 emb CAA65450.1        | kinase [Homo sapiens]                   | 217 | 6e-56 | G |
| gi 2995269 emb CAA15818.1        | MMRING3.1.1 [Mus musculus]              | 217 | 6e-56 | G |
| gi 2780779 db BAA24379.1         | Ring3 [Mus musculus] >gi 2780777...     | 217 | 6e-56 | G |
| gi 2780775 db BAA24377.1         | Ring3 [Mus musculus]                    | 217 | 6e-56 | G |
| gi 39645317 gb AAH63840.1        | BRD2 protein [Homo sapiens]             | 217 | 6e-56 | G |
| gi 1588281 prf 2208296A          | RING3 protein                           | 217 | 6e-56 |   |
| gi 1370092 emb CAA65449.1        | kinase [Gallus gallus]                  | 213 | 1e-54 |   |
| gi 3129967 emb CAA18965.1        | RING3 kinase [synthetic construc...     | 213 | 1e-54 |   |
| gi 34392374 db BAC82511.1        | Serine threonine Kinase [Coturn...      | 213 | 1e-54 |   |
| gi 54311476 gb AAH84758.1        | Brd2-A-prov protein [Xenopus lae...     | 202 | 2e-51 | G |
| gi 27696271 gb AAH43784.1        | Brd2-A-prov protein [Xenopus lae...     | 202 | 2e-51 | G |
| gi 50756877 ref XP_415337.1      | PREDICTED: similar to RING3 ki...       | 196 | 1e-49 | G |
| gi 8575733 gb AAF78072.1         | bromodomain-containing FSH-like p...    | 195 | 2e-49 | G |
| gi 11067749 ref NP_031397.1      | bromodomain containing protein...       | 195 | 2e-49 | G |
| gi 34853148 ref XP_342397.1      | similar to Brd3 protein [Rattu...       | 195 | 2e-49 | G |
| gi 21594670 gb AAH32124.1        | BRD3 protein [Homo sapiens] >gi ...     | 195 | 2e-49 | G |
| gi 31981064 ref NP_075825.2      | bromodomain containing 3 [Mus ...       | 195 | 2e-49 | G |
| gi 40788944 db BAA05393.2        | KIAA0043 [Homo sapiens]                 | 195 | 2e-49 | G |
| gi 26345416 db BAC36359.1        | unnamed protein product [Mus mu...      | 195 | 2e-49 | G |
| gi 47115837 sp Q8K2F0 BRD3 MOUSE | Bromodomain-containing pro...           | 195 | 2e-49 | G |
| gi 26332152 db BAC29806.1        | unnamed protein product [Mus mu...      | 195 | 2e-49 | G |
| gi 50757295 ref XP_425330.1      | PREDICTED: similar to bromodom...       | 193 | 9e-49 | G |
| gi 47086635 ref NP_997867.1      | Unknown (protein for MGC:77289...       | 191 | 6e-48 | G |
| gi 33416361 gb AAH55533.1        | Zgc:77289 protein [Danio rerio]         | 191 | 6e-48 | G |
| gi 33417197 gb AAH55508.1        | Unknown (protein for IMAGE:38191...     | 189 | 2e-47 |   |
| gi 33416865 gb AAH55543.1        | Unknown (protein for IMAGE:59138...     | 188 | 3e-47 |   |
| gi 19171509 emb CAC84085.1       | hypothetical protein [Takifugu ...      | 187 | 7e-47 |   |
| gi 47216871 emb CAG11678.1       | unnamed protein product [Tetrao...      | 186 | 2e-46 |   |
| gi 47212213 emb CAF94980.1       | unnamed protein product [Tetrao...      | 184 | 4e-46 |   |
| gi 7657218 ref NP_055114.1       | bromodomain-containing protein ...      | 182 | 2e-45 | G |
| gi 33879612 gb AAH30158.1        | BRD4 protein [Homo sapiens]             | 182 | 2e-45 | G |
| gi 34862361 ref XP_343176.1      | similar to bromodomain-contain...       | 182 | 2e-45 | G |
| gi 37674287 ref NP_932762.1      | bromodomain containing 4 isofo...       | 182 | 2e-45 | G |
| gi 31560788 ref NP_065254.2      | bromodomain containing 4 isofo...       | 182 | 2e-45 | G |
| gi 19718731 ref NP_490597.1      | bromodomain-containing protein...       | 182 | 2e-45 | G |
| gi 52350614 gb AAH82782.1        | Unknown (protein for IMAGE:53893...     | 182 | 2e-45 |   |
| gi 27804346 gb AAO22237.1        | BRD4-NUT fusion oncoprotein [Hom...     | 182 | 2e-45 |   |
| gi 3184498 gb AAC27978.1         | R31546_1 [Homo sapiens]                 | 182 | 2e-45 | G |

|                                  |  |     |       |   |
|----------------------------------|--|-----|-------|---|
| gi 45501005 qb AAH67129.1        | Unknown (protein for IMAGE:61387...      | 182 | 2e-45 |   |
| gi 50400639 sp Q9ESU6 BRD4 MOUSE | Bromodomain-containing pro...            | 182 | 2e-45 | G |
| gi 18157527 db BAB83842.1        | BRD2~partially supported by GEN...       | 182 | 2e-45 |   |
| gi 49118460 qb AAH73443.1        | LOC443648 protein [Xenopus laevis]       | 180 | 8e-45 | G |
| gi 45554416 ref NP_996370.1      | CG2252-PC, isoform C [Drosophi...        | 180 | 1e-44 | G |
| gi 24640482 ref NP_511078.2      | CG2252-PB, isoform B [Drosophi...        | 180 | 1e-44 | G |
| gi 24210305 emb CAD54663.1       | bromodomain containing 2 [Danio...       | 180 | 1e-44 | G |
| gi 280611 pir A43742             | female sterile homeotic protein, 205K... | 180 | 1e-44 |   |
| gi 31206311 ref XP_312107.1      | ENSANGP00000016848 [Anopheles ...        | 179 | 1e-44 | G |
| gi 55241967 qb EAA07774.2        | ENSANGP00000016848 [Anopheles ga...      | 179 | 1e-44 |   |
| gi 47210026 emb CAF90901.1       | unnamed protein product [Tetrao...       | 179 | 2e-44 |   |
| gi 47209011 emb CAF91369.1       | unnamed protein product [Tetrao...       | 179 | 2e-44 |   |
| gi 57092013 ref XP_537803.1      | PREDICTED: similar to Bromodom...        | 177 | 9e-44 |   |
| gi 49899749 qb AAH76786.1        | Brd4-prov protein [Xenopus laevis]       | 176 | 1e-43 | G |
| gi 48134425 ref XP_393347.1      | similar to ENSANGP00000016848 ...        | 176 | 1e-43 | G |
| gi 28278510 qb AAH45866.1        | Similar to bromodomain containin...      | 176 | 2e-43 |   |
| gi 10441758 qb AAG17179.1        | RING3 [Myxine glutinosa]                 | 174 | 4e-43 |   |
| gi 20302741 qb AAM18869.1        | unknown [Branchiostoma floridae]         | 171 | 5e-42 |   |
| gi 38014413 qb AAH60452.1        | LOC398944 protein [Xenopus laevis]       | 167 | 9e-41 | G |
| gi 55587546 ref XP_524767.1      | PREDICTED: similar to testis-s...        | 166 | 1e-40 |   |
| gi 28839607 qb AAH47900.1        | BRDT protein [Homo sapiens]              | 166 | 2e-40 | G |
| gi 33355659 qb AAQ16198.1        | testis-specific BRDT protein [Ho...      | 166 | 2e-40 | G |
| gi 2554915 qb AAB87862.1         | BRDT [Homo sapiens]                      | 166 | 2e-40 | G |
| gi 46399200 ref NP_997072.1      | testis-specific bromodomain pr...        | 166 | 2e-40 | G |
| gi 57088245 ref XP_537079.1      | PREDICTED: similar to testis-s...        | 163 | 1e-39 |   |
| gi 38541875 qb AAH62700.1        | BRDT protein [Homo sapiens]              | 162 | 2e-39 | G |
| gi 16905089 ref NP_473395.1      | bromodomain, testis-specific [...        | 161 | 4e-39 | G |
| gi 34875962 ref XP_223146.2      | similar to bromodomain-contain...        | 160 | 7e-39 | G |
| gi 50927337 qb AAH78999.1        | Unknown (protein for MGC:93906) ...      | 160 | 7e-39 |   |
| gi 50751326 ref XP_422346.1      | PREDICTED: similar to bromodom...        | 160 | 7e-39 | G |
| gi 47208417 emb CAF92498.1       | unnamed protein product [Tetrao...       | 160 | 1e-38 |   |
| gi 52545711 emb CAH56208.1       | hypothetical protein [Homo sapi...       | 130 | 7e-30 | G |
| gi 55648495 ref XP_512452.1      | PREDICTED: similar to bromodom...        | 128 | 5e-29 |   |
| gi 57101624 ref XP_541985.1      | PREDICTED: similar to abhydrol...        | 127 | 8e-29 |   |
| gi 47210344 emb CAF96012.1       | unnamed protein product [Tetrao...       | 124 | 5e-28 |   |
| gi 1256804 qb AAB18943.1         | RING3 protein [Xenopus laevis]           | 121 | 4e-27 |   |
| gi 25152243 ref NP_509770.2      | bromodomain containing (XL193)...        | 110 | 1e-23 | G |
| gi 7504519 pir T22845            | hypothetical protein F57C7.1a - Caen...  | 110 | 1e-23 |   |
| gi 2654068 qb AAB87684.1         | RING3 [Danio rerio]                      | 107 | 7e-23 | G |
| gi 39582126 emb CAE60803.1       | Hypothetical protein CBG04495 [...       | 107 | 1e-22 |   |
| gi 24649433 ref NP_651190.1      | CG13597-PA [Drosophila melanog...        | 104 | 7e-22 | G |
| gi 19528091 qb AAL90160.1        | AT24535p [Drosophila melanogaster]       | 104 | 7e-22 |   |
| gi 17568247 ref NP_509771.1      | bromodomain protein (XL193) [C...        | 103 | 1e-21 | G |
| gi 32564850 ref NP_871879.1      | bromodomain containing protein...        | 101 | 5e-21 | G |
| gi 17510957 ref NP_491384.1      | bromodomain containing protein...        | 101 | 5e-21 | G |
| gi 39598215 emb CAE68907.1       | Hypothetical protein CBG14881 [...       | 98  | 7e-20 |   |
| gi 55632563 ref XP_520343.1      | PREDICTED: similar to bromodom...        | 91  | 1e-17 |   |
| gi 28573564 ref NP_611401.2      | CG7229-PA [Drosophila melanoga...        | 86  | 3e-16 | G |
| gi 16604681 qb AAL24133.1        | putative kinase [Arabidopsis tha...      | 86  | 3e-16 | G |
| gi 19528087 qb AAL90158.1        | AT24439p [Drosophila melanogaster]       | 86  | 3e-16 |   |
| gi 7573452 emb CAB87766.1        | kinase-like protein [Arabidopsis...      | 86  | 3e-16 |   |

|                             |  |    |       |   |
|-----------------------------|--|----|-------|---|
| gi 9294219 dbj BAB02121.1   | unnamed protein product [Arabido...    | 85 | 6e-16 |   |
| gi 15232127 ref NP_189362.1 | DNA-binding bromodomain-contai...      | 85 | 6e-16 | G |
| gi 4581512 emb CAE40169.1   | SPCC1450.02 [Schizosaccharomyces...    | 84 | 8e-16 |   |
| gi 46438562 gb EAK97891.1   | hypothetical protein CaO19.8593 ...    | 84 | 1e-15 |   |
| gi 47201045 emb CAF89147.1  | unnamed protein product [Tetrao...     | 84 | 1e-15 |   |
| gi 27803968 gb AAO22056.1   | IMB1 [Arabidopsis thaliana] >gi ...    | 83 | 2e-15 | G |
| gi 3033396 gb AAC12830.1    | putative RING3 protein [Arabidops...   | 83 | 2e-15 |   |
| gi 42571057 ref NP_973602.1 | DNA-binding bromodomain-contai...      | 83 | 2e-15 | G |
| gi 20259928 gb AAM13311.1   | unknown protein [Arabidopsis tha...    | 83 | 2e-15 |   |
| gi 56236042 gb AAV84477.1   | At1g73150 [Arabidopsis thaliana]...    | 82 | 4e-15 | G |
| gi 50253452 gb AAF71928.1   | At5g63330 [Arabidopsis thaliana]...    | 81 | 7e-15 | G |
| gi 50940753 ref XP_479904.1 | putative bromodomain-containin...      | 80 | 2e-14 | G |
| gi 19114532 ref NP_593620.1 | protein with 2 bromodomains, p...      | 80 | 2e-14 | G |
| gi 17551634 ref NP_508124.1 | kinase (40.9 kD) (XB213) [Caen...      | 79 | 3e-14 | G |
| gi 57282320 emb CAD43286.1  | bromodomain-containing RNA-bind...     | 79 | 3e-14 |   |
| gi 49652967 emb CAG85306.1  | unnamed protein product [Debary...     | 79 | 3e-14 | G |
| gi 7671448 emb CAB89388.1   | bromodomain protein-like [Arabid...    | 79 | 3e-14 | G |
| gi 19173489 ref NP_597292.1 | GENERAL TRANSCRIPTION FACTOR [...]     | 79 | 3e-14 | G |
| gi 39592569 emb CAE63646.1  | Hypothetical protein CBG08144 [...]    | 79 | 3e-14 |   |
| gi 13186138 emb CAC33451.1  | PSTVd RNA-biding protein, Virpl...     | 79 | 4e-14 |   |
| gi 34874095 ref XP_221050.2 | similar to fetal Alzheimer ant...      | 78 | 6e-14 | G |
| gi 54635558 gb EAL24961.1   | GA15830-PA [Drosophila pseudoobs...    | 78 | 6e-14 |   |
| gi 57282318 emb CAD43285.1  | bromodomain-containing RNA-bind...     | 78 | 6e-14 |   |
| gi 57090969 ref XP_537586.1 | PREDICTED: similar to fetal Al...      | 78 | 7e-14 |   |
| gi 30046988 gb AAH50566.1   | FALZ protein [Homo sapiens]            | 78 | 7e-14 | G |
| gi 31322942 gb AAF22284.1   | bromodomain PHD finger transcrip...    | 78 | 7e-14 | G |
| gi 30793995 gb AAF40447.1   | unknown protein [Arabidopsis tha...    | 78 | 7e-14 | G |
| gi 55645849 ref XP_511643.1 | PREDICTED: hypothetical protei...      | 78 | 7e-14 |   |
| gi 38788274 ref NP_872579.2 | fetal Alzheimer antigen isoform...     | 78 | 7e-14 | G |
| gi 38788260 ref NP_004450.3 | fetal Alzheimer antigen isoform...     | 78 | 7e-14 | G |
| gi 8978291 dbj BAA98182.1   | unnamed protein product [Arabido...    | 78 | 7e-14 |   |
| gi 45595651 gb AAH67234.1   | FALZ protein [Homo sapiens]            | 78 | 7e-14 | G |
| gi 7428977 pir S71788       | P/CAF protein - human                  | 78 | 7e-14 |   |
| gi 6683492 dbj BAA89208.1   | bromodomain PHD finger transcrip...    | 78 | 7e-14 | G |
| gi 38174486 gb AAH60715.1   | Falz protein [Mus musculus]            | 77 | 1e-13 | G |
| gi 18204482 gb AAH21489.1   | Falz protein [Mus musculus]            | 77 | 1e-13 | G |
| gi 31216247 ref XP_316196.1 | ENSANGP00000005931 [Anopheles ...]     | 77 | 1e-13 | G |
| gi 6016737 gb AAF01563.1    | hypothetical protein [Arabidopsis...   | 77 | 1e-13 |   |
| gi 57282316 emb CAD43284.1  | bromodomain-containing RNA-bind...     | 77 | 1e-13 |   |
| gi 51766499 ref XP_126724.5 | fetal Alzheimer antigen [Mus m...      | 77 | 1e-13 | G |
| gi 22136456 gb AAM91306.1   | unknown protein [Arabidopsis tha...    | 77 | 1e-13 | G |
| gi 24654644 ref NP_728507.1 | CG32346-PA, isoform A [Drosoph...      | 77 | 1e-13 | G |
| gi 24654638 ref NP_728505.1 | CG32346-PB, isoform B [Drosoph...      | 77 | 1e-13 | G |
| gi 57282322 emb CAD43287.1  | bromodomain-containing RNA-bind...     | 77 | 1e-13 |   |
| gi 28516430 ref XP_284106.1 | similar to PCAF acetyltransfer...      | 77 | 1e-13 | G |
| gi 16265798 gb AAL16644.1   | nucleosome remodeling factor lar...    | 77 | 1e-13 |   |
| gi 48104118 ref XP_395718.1 | similar to fetal Alzheimer ant...      | 77 | 1e-13 | G |
| gi 11359006 pir T42517      | bromodomain protein - fission yeast... | 77 | 1e-13 |   |
| gi 25406905 pir A86198      | hypothetical protein [imported] - A... | 77 | 1e-13 | G |
| gi 40805843 ref NP_003875.3 | p300/CBP-associated factor [Ho...      | 77 | 2e-13 | G |

|                                 |  |    |       |   |
|---------------------------------|--|----|-------|---|
| gi 57103570 ref XP_534249.1     | PREDICTED: similar to p300/CBP...        | 77 | 2e-13 |   |
| gi 55619933 ref XP_516321.1     | PREDICTED: similar to p300/CBP...        | 77 | 2e-13 |   |
| gi 50937581 ref XP_478318.1     | putative RING3 protein [Oryza ...        | 77 | 2e-13 | G |
| gi 23297757 gb AAN13019.1       | unknown protein [Arabidopsis tha...      | 77 | 2e-13 | G |
| gi 50733046 ref XP_426001.1     | PREDICTED: similar to PCAF [Ga...        | 77 | 2e-13 | G |
| gi 27574121 pdb 1N72 A          | Chain A, Structure And Ligand Of A H...  | 77 | 2e-13 | S |
| gi 25511645 pir H86312          | F2H15.2 protein - Arabidopsis thali...   | 77 | 2e-13 |   |
| gi 14317910 dbj BAE59138.1      | PCAF [Gallus gallus]                     | 77 | 2e-13 | G |
| gi 34874275 ref XP_217321.2     | similar to PCAF acetyltransfer...        | 76 | 2e-13 | G |
| gi 31209509 ref XP_313721.1     | ENSANGP00000003808 [Anopheles ...        | 76 | 2e-13 | G |
| gi 34903950 ref NP_913322.1     | putative PSTVd RNA-biding prot...        | 76 | 2e-13 | G |
| gi 49650060 emb CAG79786.1      | unnamed protein product [Yarrow...       | 76 | 2e-13 | G |
| gi 47221861 emb CAF98873.1      | unnamed protein product [Tetrao...       | 76 | 2e-13 |   |
| gi 15810439 gb AAL07107.1       | unknown protein [Arabidopsis tha...      | 76 | 3e-13 |   |
| gi 57282314 emb CAD43283.1      | bromodomain-containing RNA-bind...       | 76 | 3e-13 |   |
| gi 50757845 ref XP_415674.1     | PREDICTED: similar to fetal Al...        | 76 | 3e-13 | G |
| gi 435855 gb AAB28651.1         | CREB-binding protein; CBP [Mus sp....    | 75 | 4e-13 | G |
| gi 737920 prf  1923401A         | protein CBP                              | 75 | 4e-13 |   |
| gi 47223942 emb CAG06119.1      | unnamed protein product [Tetrao...       | 75 | 5e-13 |   |
| gi 38099205 gb EAA46582.1       | hypothetical protein MG08925.4 [...      | 75 | 6e-13 | G |
| gi 50345997 ref NP_001420.2     | E1A binding protein p300 [Homo...        | 74 | 8e-13 | G |
| gi 3024341 sp Q09472 P300 HUMAN | E1A-associated protein p300...           | 74 | 8e-13 | G |
| gi 6320132 ref NP_010213.1      | Protein involved in transcripti...       | 74 | 8e-13 | G |
| gi 31753089 gb AAH53889.1       | EP300 protein [Homo sapiens]             | 74 | 8e-13 | G |
| gi 57092731 ref XP_531721.1     | PREDICTED: similar to E1A-asso...        | 74 | 8e-13 |   |
| gi 56118232 ref NP_808489.3     | E1A binding protein p300 [Mus ...        | 74 | 8e-13 |   |
| gi 55661272 ref XP_515155.1     | PREDICTED: E1A binding protein...        | 74 | 8e-13 |   |
| gi 48094965 ref XP_394317.1     | similar to ENSANGP00000004748 ...        | 74 | 8e-13 | G |
| gi 4321116 gb AAC51331.2        | CREB-binding protein [Homo sapiens]      | 74 | 1e-12 | G |
| gi 6321691 ref NP_011768.1      | Histone acetyltransferase, acet...       | 74 | 1e-12 | G |
| gi 38505359 gb AAR23149.1       | CREB-binding protein [Rattus nor...      | 74 | 1e-12 | G |
| gi 57088067 ref XP_536991.1     | PREDICTED: similar to CREB-bin...        | 74 | 1e-12 |   |
| gi 4758056 ref NP_004371.1      | CREB binding protein [Homo sapi...       | 74 | 1e-12 | G |
| gi 55249595 gb AAH86282.1       | Unknown (protein for MGC:83709) ...      | 74 | 1e-12 |   |
| gi 51769561 ref XP_148699.4     | CREB binding protein [Mus musc...        | 74 | 1e-12 | G |
| gi 51769419 ref XP_489497.1     | similar to CREB-binding protei...        | 74 | 1e-12 | G |
| gi 51013881 gb AAT93234.1       | YGR252W [Saccharomyces cerevisiae]       | 74 | 1e-12 |   |
| gi 50728690 ref XP_416238.1     | PREDICTED: similar to E1A-asso...        | 74 | 1e-12 | G |
| gi 19547887 gb AAL87532.1       | CREB-binding protein [Mus muscul...      | 74 | 1e-12 | G |
| gi 49117594 gb AAH72594.1       | Unknown (protein for IMAGE:64084...      | 74 | 1e-12 |   |
| gi 21307831 gb AAL54859.1       | CREB-binding protein [Aplysia ca...      | 74 | 1e-12 |   |
| gi 1502355 emb CAA67614.1       | GCN5 [Saccharomyces cerevisiae]          | 74 | 1e-12 |   |
| gi 47217876 emb CAG02369.1      | unnamed protein product [Tetrao...       | 74 | 1e-12 |   |
| gi 631119 pir  S39162           | transcription coactivator CREB-bindin... | 74 | 1e-12 |   |
| gi 23200188 pdb 1JSP B          | Chain B, Nmr Structure Of Cbp Bromod...  | 74 | 1e-12 | S |
| gi 11513447 pdb 1E61 A          | Chain A, Bromodomain From Gcn5 Compl...  | 74 | 1e-12 | S |
| gi 24659254 ref NP_726307.1     | CG30417-PA [Drosophila melanog...        | 74 | 1e-12 | G |
| gi 46227211 gb EAK88161.1       | protein with 4 ankyrin repeats p...      | 74 | 1e-12 |   |
| gi 50755982 ref XP_414964.1     | PREDICTED: similar to CREB-bin...        | 74 | 1e-12 | G |
| gi 54636653 gb EAL35582.1       | hypothetical protein Chro.50328 ...      | 74 | 1e-12 |   |

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|-----------------------------|---|----|-------|---|
| gi 5468533 gb AAC50890.2    | p300/CBP-associated factor [Homo ...    | 74 | 1e-12 | G |
| gi 44983942 gb AAS52978.1   | AER297Cp [Ashbya gossypii ATCC 1...     | 73 | 2e-12 | G |
| gi 52345413 ref NP_064389.2 | p300/CBP-associated factor [Mu...       | 73 | 2e-12 | G |
| gi 49649342 emb CAG79052.1  | YlGCN5 [Yarrowia lipolytica CLI...      | 73 | 2e-12 | G |
| gi 50287799 ref XP_446329.1 | unnamed protein product [Candi...       | 73 | 2e-12 | G |
| gi 7862148 gb AAF70498.1    | PCAF acetyltransferase; p300/CBP-...    | 73 | 2e-12 | G |
| gi 44983653 gb AAS52752.1   | AER068Cp [Ashbya gossypii ATCC 1...     | 73 | 2e-12 | G |
| gi 8885596 db SAA97526.1    | unnamed protein product [Arabido...     | 73 | 2e-12 |   |
| gi 26451383 db BAC42791.1   | unknown protein [Arabidopsis th...      | 73 | 2e-12 | G |
| gi 54641233 gb EAL29983.1   | GAL6840-PA [Drosophila pseudoobs...     | 72 | 3e-12 |   |
| gi 50303459 ref XP_451671.1 | unnamed protein product [Kluyv...       | 72 | 3e-12 | G |
| gi 47229415 emb CAF99403.1  | unnamed protein product [Tetrao...      | 72 | 4e-12 |   |
| gi 40744729 gb EAA63885.1   | hypothetical protein AN1984.2 [A...     | 72 | 5e-12 | G |
| gi 311664 emb CAA79377.1    | BDF1 [Saccharomyces cerevisiae]         | 71 | 7e-12 |   |
| gi 608567 gb AAA89115.1     | Bdflp                                   | 71 | 7e-12 |   |
| gi 6323431 ref NP_013503.1  | Protein involved in transcripti...      | 71 | 7e-12 | G |
| gi 31204369 ref XP_311133.1 | ENSANGP00000004748 [Anopheles ...       | 71 | 7e-12 | G |
| gi 24663348 ref NP_648586.2 | CG4107-PA [Drosophila melanoga...       | 71 | 7e-12 | G |
| gi 54642162 gb EAL30911.1   | GAL7962-PA [Drosophila pseudoobs...     | 71 | 7e-12 |   |
| gi 55243803 gb EAA06516.3   | ENSANGP00000004748 [Anopheles ga...     | 71 | 7e-12 |   |
| gi 55243802 gb EAL41310.1   | ENSANGP00000025904 [Anopheles ga...     | 71 | 7e-12 |   |
| gi 45383496 ref NP_989660.1 | GCN5 general control of amino-...       | 71 | 7e-12 | G |
| gi 50285717 ref XP_445287.1 | unnamed protein product [Candi...       | 71 | 7e-12 | G |
| gi 3211728 gb AAC39102.1    | GCN5; HAT [Drosophila melanogaster]     | 71 | 7e-12 |   |
| gi 38099365 gb EAA46722.1   | hypothetical protein MG09943.4 [...     | 71 | 7e-12 | G |
| gi 39590738 emb CAE65110.1  | Hypothetical protein CBG09974 [...      | 71 | 7e-12 |   |
| gi 47208228 emb CAF96470.1  | unnamed protein product [Tetrao...      | 70 | 1e-11 |   |
| gi 54642704 gb EAL31449.1   | GAL3644-PA [Drosophila pseudoobs...     | 70 | 2e-11 |   |
| gi 19115719 ref NP_594807.1 | putative yeast transcriptional...       | 70 | 2e-11 | G |
| gi 17533491 ref NP_496998.1 | bromodomain PHD finger transcr...       | 70 | 2e-11 | G |
| gi 17533489 ref NP_496997.1 | bromodomain PHD finger transcr...       | 70 | 2e-11 | G |
| gi 17533487 ref NP_496996.1 | bromodomain PHD finger transcr...       | 70 | 2e-11 | G |
| gi 24640863 ref NP_524642.2 | CG15319-PB [Drosophila melanog...       | 70 | 2e-11 | G |
| gi 31432077 gb AAP53762.1   | contains similarity to histone a...     | 70 | 2e-11 | G |
| gi 54110963 emb CAH60782.1  | Hypothetical protein F26H11.2g ...      | 70 | 2e-11 |   |
| gi 50507802 emb CAH04722.1  | Hypothetical protein F26H11.2c ...      | 70 | 2e-11 |   |
| gi 34364498 emb CAB54234.3  | Hypothetical protein F26H11.2d ...      | 70 | 2e-11 |   |
| gi 7499972 pir T21435       | hypothetical protein F26H11.3c - Cae... | 70 | 2e-11 |   |
| gi 26350027 db BAC38653.1   | unnamed protein product [Mus mu...      | 69 | 3e-11 | G |
| gi 29569106 gb AAO84020.1   | global transcription factor grou...     | 69 | 3e-11 |   |
| gi 50302579 ref XP_451225.1 | unnamed protein product [Kluyv...       | 69 | 3e-11 | G |
| gi 12321252 gb AAG50696.1   | hypothetical protein [Arabidopsi...     | 69 | 3e-11 | G |
| gi 7511830 pir T13828       | CREB-binding protein homolog - fruit... | 69 | 4e-11 |   |
| gi 32400806 gb AAP80635.1   | histone acetyltransferase [Triti...     | 68 | 6e-11 |   |
| gi 31711984 gb AAP68348.1   | At3g54610 [Arabidopsis thaliana]...     | 68 | 6e-11 | G |
| gi 7258364 emb CAB77581.1   | histon acetyltransferase HAT1 [A...     | 68 | 6e-11 |   |
| gi 47226142 emb CAG04516.1  | unnamed protein product [Tetrao...      | 68 | 6e-11 |   |
| gi 47218844 emb CAG02829.1  | unnamed protein product [Tetrao...      | 68 | 6e-11 |   |
| gi 46433121 gb EAK92574.1   | likely histone acetyltransferase...     | 68 | 8e-11 |   |
| gi 54638697 gb EAL28099.1   | GAL5159-PA [Drosophila pseudoobs...     | 68 | 8e-11 |   |
| gi 56468960 gb EAL46759.1   | bromodomain protein, putative [E...     | 68 | 8e-11 |   |

|                             |   |    |       |   |
|-----------------------------|---|----|-------|---|
| gi 55297001 db BAD68476.1   | DNA-binding bromodomain-contain...      | 68 | 8e-11 |   |
| gi 24651761 ref NP_536734.2 | CG1966-PA [Drosophila melanoga...       | 67 | 1e-10 | G |
| gi 57228236 gb AAW44693.1   | conserved hypothetical protein [...     | 67 | 1e-10 |   |
| gi 31224454 ref XP_317442.1 | ENSANGP00000011787 [Anopheles ...       | 67 | 1e-10 | G |
| gi 50256825 gb EAL19543.1   | hypothetical protein CNBG1720 [C...     | 67 | 1e-10 |   |
| gi 55237658 gb EAA12387.2   | ENSANGP00000011787 [Anopheles ga...     | 67 | 1e-10 |   |
| gi 16768864 gb AAL28651.1   | LD09043p [Drosophila melanogaster]      | 67 | 1e-10 |   |
| gi 68563666 gb AAF29981.1   | histone acetyltransferase GCN5 [T...    | 67 | 1e-10 |   |
| gi 5031520 gb AAD38202.1    | histone acetyltransferase GCN5 [T...    | 67 | 1e-10 |   |
| gi 5059246 gb AAD38952.1    | ATP-dependent chromatin assembly ...    | 67 | 1e-10 |   |
| gi 38105685 gb EAA52082.1   | hypothetical protein MG03677.4 [...     | 67 | 1e-10 | G |
| gi 7635502 emb CAB88669.1   | chromatin accessibility complex ...     | 67 | 1e-10 |   |
| gi 13183793 gb AAK15343.1   | CECR2 protein [Homo sapiens] >gi...     | 67 | 1e-10 | G |
| gi 17552708 ref NP_499161.1 | CBP/p300 homolog (cbp-1) [Caen...       | 67 | 1e-10 | G |
| gi 17552710 ref NP_499160.1 | CBP/p300 homolog (cbp-1) [Caen...       | 67 | 1e-10 | G |
| gi 52545926 emb CAH56122.1  | hypothetical protein [Homo sapi...      | 67 | 1e-10 | G |
| gi 2133462 pir S60123       | hypothetical protein R10E11.1 - Caen... | 67 | 1e-10 |   |
| gi 12698025 db BAB21831.1   | KIAA1740 protein [Homo sapiens]         | 67 | 1e-10 | G |
| gi 33242492 gb AAQ00945.1   | general control nonrepressed 5 [...     | 67 | 2e-10 |   |
| gi 57106607 ref XP_534935.1 | PREDICTED: similar to Cat eye ...       | 67 | 2e-10 |   |
| gi 50910201 ref XP_466589.1 | putative global transcription ...       | 67 | 2e-10 | G |
| gi 51979260 ref XP_507492.1 | PREDICTED OJ1791_B03.42-1 gene...       | 67 | 2e-10 | G |
| gi 13699186 db BAB41205.1   | kinase-like protein [Oryza sativa]      | 67 | 2e-10 |   |
| gi 17017400 gb AAL33654.1   | histone acetyl transferase [Zea ...     | 66 | 2e-10 |   |
| gi 50729022 ref XP_416392.1 | PREDICTED: similar to KIAA1740...       | 66 | 2e-10 | G |
| gi 50728910 ref XP_416340.1 | PREDICTED: similar to Transcri...       | 66 | 2e-10 | G |
| gi 48105414 ref XP_393011.1 | similar to CG32394-PA [Apis me...       | 66 | 2e-10 | G |
| gi 40740639 gb EAA59829.1   | conserved hypothetical protein [...     | 65 | 4e-10 | G |
| gi 51717063 ref XP_204234.3 | cat eye syndrome chromosome re...       | 65 | 4e-10 | G |
| gi 51714476 ref XP_489839.1 | similar to Cat eye syndrome cr...       | 65 | 4e-10 | G |
| gi 10045561 emb CAC07919.1  | putative protein [Arabidopsis t...      | 65 | 4e-10 | G |
| gi 17534715 ref NP_494767.1 | bromodomain adjacent zinc fing...       | 65 | 5e-10 | G |
| gi 49658230 emb CAG91071.1  | unnamed protein product [Debary...      | 65 | 5e-10 | G |
| gi 47230592 emb CAF99785.1  | unnamed protein product [Tetrao...      | 65 | 5e-10 |   |
| gi 2267585 gb AAB63585.1    | transcription intermediary factor...    | 65 | 5e-10 | G |
| gi 998813 gb AAB34289.1     | TIF1 [Mus sp.]                          | 65 | 6e-10 | G |
| gi 42546847 gb EAA69690.1   | conserved hypothetical protein [...     | 65 | 6e-10 | G |
| gi 34391523 gb AAN61105.1   | putative chromatin remodelling f...     | 65 | 6e-10 | G |
| gi 32417982 ref XP_329469.1 | hypothetical protein [Neurospo...       | 65 | 6e-10 | G |
| gi 34328067 ref NP_659542.1 | tripartite motif protein 24 [M...       | 65 | 6e-10 | G |
| gi 56473058 gb EAL50506.1   | bromodomain protein, putative [E...     | 65 | 6e-10 |   |
| gi 38110007 gb EAA55792.1   | hypothetical protein MG01443.4 [...     | 65 | 6e-10 | G |
| gi 19343832 gb AAH25482.1   | Trim24 protein [Mus musculus]           | 65 | 6e-10 | G |
| gi 51094800 gb EAL24046.1   | transcriptional intermediary fac...     | 64 | 8e-10 | G |
| gi 51094801 gb EAL24047.1   | transcriptional intermediary fac...     | 64 | 8e-10 | G |
| gi 55629844 ref XP_519502.1 | PREDICTED: transcriptional int...       | 64 | 8e-10 |   |
| gi 47211977 emb CAF95299.1  | unnamed protein product [Tetrao...      | 64 | 8e-10 |   |
| gi 32420965 ref XP_330926.1 | hypothetical protein [Neurospo...       | 64 | 1e-09 | G |
| gi 25058961 gb AAH39907.1   | GCN5 general control of amino-ac...     | 64 | 1e-09 | G |



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|--------------------------------|---|----|-------|---|
| gi 34873737 ref XP_239340.2    | similar to GCN5 general contro...       | 64 | 1e-09 | G |
| gi 57091497 ref XP_548094.1    | PREDICTED: similar to GCN5 gen...       | 64 | 1e-09 |   |
| gi 31204491 ref XP_311194.1    | ENSANGP00000001532 [Anopheles ...       | 64 | 1e-09 | G |
| gi 55645415 ref XP_511500.1    | PREDICTED: similar to GCN5 gen...       | 64 | 1e-09 | G |
| gi 10835101 ref NP_066564.1    | GCN5 general control of amino-...       | 64 | 1e-09 | G |
| gi 39795334 gb AAH63752.1      | General control of amino acid sy...     | 64 | 1e-09 | G |
| gi 37811671 gb AAP03834.1      | general control of amino-acid sy...     | 64 | 1e-09 |   |
| gi 1911495 gb AAB50690.1       | hGCN5=transcriptional adaptor [hu...    | 64 | 1e-09 |   |
| gi 13278322 gb AAH03983.1      | Gcn5l2 protein [Mus musculus]           | 64 | 1e-09 | G |
| gi 12084461 pdb 1F68 A         | Chain A, Nmr Solution Structure Of T... | 64 | 1e-09 |   |
| gi 46228118 gb EAK89017.1      | GCN5 like acetylase + bromodoma...      | 63 | 2e-09 |   |
| gi 54658191 gb EAL36865.1      | histone acetyltransferase [Crypt...     | 63 | 2e-09 |   |
| gi 48094754 ref XP_392182.1    | similar to ENSANGP00000020172 ...       | 63 | 2e-09 | G |
| gi 1245146 gb AAB01099.1       | HAT A1                                  | 63 | 2e-09 |   |
| gi 51979535 ref XP_507560.1    | PREDICTED P0007D08.15 gene pro...       | 63 | 2e-09 | G |
| gi 28829334 gb AAO51876.1      | similar to Dictyostelium discoid...     | 63 | 2e-09 |   |
| gi 31210237 ref XP_314085.1    | ENSANGP000000003691 [Anopheles ...      | 62 | 3e-09 | G |
| gi 34911780 ref NP_917237.1    | OJ1316_H05.17 [Oryza sativa (j...       | 62 | 3e-09 | G |
| gi 9910238 ref NP_064388.1     | general control of amino acid s...      | 62 | 3e-09 | G |
| gi 55240574 gb EAA09379.3      | ENSANGP000000003691 [Anopheles ga...    | 62 | 3e-09 |   |
| gi 55296880 db BAD68333.1      | PSTVd RNA-binding protein-like [...     | 62 | 3e-09 |   |
| gi 29248585 gb EAA40115.1      | GLP_80_20751_21473 [Giardia lamb...     | 62 | 3e-09 |   |
| gi 14165484 gb AAH08039.1      | BRD8 protein [Homo sapiens] >gi ...     | 62 | 5e-09 | G |
| gi 34452709 ref NP_899203.1    | bromodomain containing 8 isofo...       | 62 | 5e-09 | G |
| gi 21536234 ref NP_084423.1    | bromodomain containing 8 [Mus ...       | 62 | 5e-09 | G |
| gi 34452707 ref NP_631938.1    | bromodomain containing 8 isofo...       | 62 | 5e-09 | G |
| gi 2135974 pir S68142          | probable transcription factor SMAP -... | 62 | 5e-09 | G |
| gi 42554923 gb EAA77766.1      | hypothetical protein FG09717.1 [...     | 62 | 5e-09 | G |
| gi 57093561 ref XP_531918.1    | PREDICTED: similar to bromodom...       | 62 | 5e-09 |   |
| gi 56606080 ref NP_001008509.1 | bromodomain containing 8 [R...          | 62 | 5e-09 |   |
| gi 34452705 ref NP_006687.3    | bromodomain containing 8 isofo...       | 62 | 5e-09 | G |
| gi 18606031 gb AAH23160.1      | Brd8 protein [Mus musculus]             | 62 | 5e-09 | G |
| gi 55732238 emb CAH92823.1     | hypothetical protein [Pongo pyg...      | 62 | 5e-09 |   |
| gi 2707336 gb AAB92257.1       | histone acetyltransferase [Arabid...    | 62 | 5e-09 |   |
| gi 2655006 gb AAB87858.1       | thyroid hormone receptor coactiva...    | 62 | 5e-09 | G |
| gi 57525007 ref NP_001006148.1 | similar to bromodomain cont...          | 61 | 7e-09 |   |
| gi 34854705 ref XP_229225.2    | similar to KIAA1476 protein [R...       | 61 | 7e-09 | G |
| gi 50754923 ref XP_414542.1    | PREDICTED: similar to bromodom...       | 61 | 7e-09 | G |
| gi 53136534 emb CAG32596.1     | hypothetical protein [Gallus ga...      | 61 | 7e-09 | G |
| gi 26328143 db BAC27812.1      | unnamed protein product [Mus mu...      | 61 | 7e-09 | G |
| gi 57222786 gb AAW40830.1      | transcriptional activator gcn5, ...     | 61 | 9e-09 |   |
| gi 50261018 gb EAL23668.1      | hypothetical protein CNBA3150 [C...     | 61 | 9e-09 |   |
| gi 54635725 gb EAL25128.1      | GA10623-PA [Drosophila pseudoobs...     | 61 | 9e-09 |   |
| gi 57097415 ref XP_532754.1    | PREDICTED: similar to transcri...       | 60 | 1e-08 |   |
| gi 55238947 gb EAL40012.1      | ENSANGP00000029642 [Anopheles ga...     | 60 | 1e-08 |   |
| gi 19074752 ref NP_586258.1    | TRANSCRIPTIONAL ACTIVATOR [Enc...       | 60 | 2e-08 | G |
| gi 27503567 gb AAH42646.1      | BC053917 protein [Mus musculus]         | 60 | 2e-08 | G |
| gi 46433516 gb EAK92953.1      | potential chromatin-associated p...     | 60 | 2e-08 |   |
| gi 56472259 gb EAL49757.1      | bromodomain protein, putative [E...     | 60 | 2e-08 |   |
| gi 56468123 gb EAL46008.1      | bromodomain protein, putative [E...     | 60 | 2e-08 |   |
| gi 15778343 gb AAL07393.1      | CECR2B [Homo sapiens]                   | 60 | 2e-08 | G |



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|----------------------------------|--|----|-------|---|
| gi 56518510 emb CAH76159.1       | histone acetyltransferase Gcn5,...       | 59 | 3e-08 |   |
| gi 56499474 emb CAH95151.1       | histone acetyltransferase Gcn5,...       | 59 | 3e-08 |   |
| gi 24370476 emb CAC70157.1       | polybromodomain protein [Brugia...       | 59 | 3e-08 |   |
| gi 24370475 emb CAC70156.1       | polybromodomain protein [Brugia...       | 59 | 3e-08 |   |
| gi 23491055 gb EAA22686.1        | similar to S. cerevisiae BDF1 [P...      | 59 | 3e-08 |   |
| gi 23490365 gb EAA22160.1        | histone acetyltransferase GCN5-r...      | 59 | 3e-08 |   |
| gi 38503467 gb AAR22527.1        | histone acetyltransferase [Plasm...      | 59 | 4e-08 |   |
| gi 23612782 ref NP_704321.1      | histone acetyltransferase Gcn5...        | 59 | 4e-08 | G |
| gi 7304923 ref NP_038478.1       | bromodomain adjacent to zinc fi...       | 59 | 4e-08 | G |
| gi 46098556 gb EAK83789.1        | hypothetical protein UM02619.1 [...      | 59 | 4e-08 |   |
| gi 45382753 ref NP_990008.1      | extracellular matrix protein F...        | 59 | 4e-08 | G |
| gi 29421196 dbj BAA96000.2       | KIAA1476 protein [Homo sapiens]          | 59 | 4e-08 | G |
| gi 47220585 emb CAG05611.1       | unnamed protein product [Tetrao...       | 59 | 4e-08 |   |
| gi 39598267 emb CAF68959.1       | Hypothetical protein CBG14939 [...       | 59 | 4e-08 |   |
| gi 5262644 emb CAB45759.1        | hypothetical protein [Homo sapie...      | 59 | 4e-08 | G |
| gi 22653668 sp Q9UIF8 BA2B HUMAN | Bromodomain adjacent to zi...            | 59 | 4e-08 | G |
| gi 55612288 ref XP_525949.1      | PREDICTED: bromodomain adjacen...        | 59 | 5e-08 |   |
| gi 23508131 ref NP_700801.1      | hypothetical protein PF10_0328...        | 58 | 6e-08 | G |
| gi 56472529 gb EAL50010.1        | bromodomain protein, putative [E...      | 58 | 6e-08 |   |
| gi 46226948 gb EAK87914.1        | chromodomain-helicase-DNA-bindin...      | 58 | 6e-08 |   |
| gi 54657614 gb EAL36361.1        | RIKEN cDNA A730019I05 gene [Cryp...      | 58 | 6e-08 |   |
| gi 54657612 gb EAL36360.1        | hypothetical protein Chro.20286 ...      | 58 | 8e-08 |   |
| gi 45551085 ref NP_725062.2      | CG10897-PB, isoform B [Drosoph...        | 57 | 1e-07 | G |
| gi 24652776 ref NP_725061.1      | CG10897-PD, isoform D [Drosoph...        | 57 | 1e-07 | G |
| gi 24652774 ref NP_725060.1      | CG10897-PC, isoform C [Drosoph...        | 57 | 1e-07 | G |
| gi 22023997 ref NP_523701.2      | CG10897-PA, isoform A [Drosoph...        | 57 | 1e-07 | G |
| gi 12642598 gb AAK00302.1        | Toutatis [Drosophila melanogaster]       | 57 | 1e-07 |   |
| gi 56501185 emb CAF98647.1       | hypothetical protein PB001232.0...       | 57 | 1e-07 |   |
| gi 26326149 dbj BAC26818.1       | unnamed protein product [Mus mu...       | 57 | 1e-07 | G |
| gi 57228880 gb AAW45314.1        | conserved hypothetical protein [...      | 57 | 1e-07 |   |
| gi 57087477 ref XP_536845.1      | PREDICTED: similar to bromodom...        | 57 | 1e-07 |   |
| gi 50256505 gb EAL19230.1        | hypothetical protein CNBH3290 [C...      | 57 | 1e-07 |   |
| gi 47086497 ref NP_997942.1      | Unknown (protein for MGC:66249...        | 57 | 1e-07 | G |
| gi 56474427 gb EAL51797.1        | bromodomain protein, putative [E...      | 57 | 1e-07 |   |
| gi 28277586 gb AAH44181.1        | Brd8 protein [Danio rerio]               | 57 | 1e-07 | G |
| gi 19113148 ref NP_596356.1      | putative transcriptional activ...        | 57 | 2e-07 | G |
| gi 50749002 ref XP_426440.1      | PREDICTED: similar to bromodom...        | 57 | 2e-07 | G |
| gi 47211530 emb CAF90136.1       | unnamed protein product [Tetrao...       | 57 | 2e-07 |   |
| gi 20357588 ref NP_620278.1      | TBP-associated factor 1 isofo...         | 56 | 2e-07 | G |
| gi 34865213 ref XP_234156.2      | similar to chromatin remodelin...        | 56 | 2e-07 | G |
| gi 20357585 ref NP_004597.2      | TBP-associated factor 1 isofo...         | 56 | 2e-07 | G |
| gi 34481757 emb CAD70493.2       | putative DYT3 protein [Homo sap...       | 56 | 2e-07 | G |
| gi 34481755 emb CAD70492.2       | putative DYT3 protein [Homo sap...       | 56 | 2e-07 | G |
| gi 34481753 emb CAD70491.2       | putative DYT3 protein [Homo sap...       | 56 | 2e-07 | G |
| gi 34481733 emb CAD87527.1       | putative DYT3 protein [Homo sap...       | 56 | 2e-07 | G |
| gi 47214801 emb CAF89628.1       | unnamed protein product [Tetrao...       | 56 | 2e-07 |   |
| gi 47206036 emb CAF91716.1       | unnamed protein product [Tetrao...       | 56 | 2e-07 |   |
| gi 47205952 emb CAF90865.1       | unnamed protein product [Tetrao...       | 56 | 2e-07 |   |
| gi 39582716 emb CAF65922.1       | Hypothetical protein CBG11090 [...       | 56 | 2e-07 |   |
| gi 8569258 pdb 1EQF A            | Chain A, Crystal Structure Of The Dou... | 56 | 2e-07 |   |
| gi 14670392 ref NP_115784.1      | bromodomain adjacent to zinc f...        | 56 | 3e-07 | G |

|                                  |                                      |    |       |   |
|----------------------------------|--------------------------------------|----|-------|---|
| gi 17510001 ref NP_491173.1      | histone acetyltransferase (88....    | 56 | 3e-07 | G |
| gi 57112471 ref XP_549070.1      | PREDICTED: similar to TBP-asso...    | 56 | 3e-07 |   |
| gi 31198613 ref XP_308254.1      | ENSANGP00000010809 [Anopheles ...    | 56 | 3e-07 | G |
| gi 6683496 dbj BAA89210.1        | bromodomain adjacent to zinc fin...  | 56 | 3e-07 | G |
| gi 33589500 gb AAQ22517.1        | LD26355p [Drosophila melanogaster]   | 56 | 3e-07 |   |
| gi 24649782 ref NP_651286.1      | CG11375-PA [Drosophila melanog...    | 56 | 3e-07 | G |
| gi 55639437 ref XP_509537.1      | PREDICTED: similar to KIAA0314...    | 56 | 3e-07 |   |
| gi 55628708 ref XP_527780.1      | PREDICTED: hypothetical protei...    | 56 | 3e-07 |   |
| gi 55245294 gb EAL41745.1        | ENSANGP00000028929 [Anopheles ga...  | 56 | 3e-07 |   |
| gi 55245293 gb EAA03942.2        | ENSANGP00000010809 [Anopheles ga...  | 56 | 3e-07 |   |
| gi 46103752 ref XP_395639.1      | similar to ENSANGP00000003310 ...    | 56 | 3e-07 | G |
| gi 4165087 gb AAD08675.1         | Williams-Beuren syndrome deletion... | 56 | 3e-07 | G |
| gi 47223904 emb CAG06081.1       | unnamed protein product [Tetrao...   | 56 | 3e-07 |   |
| gi 32967603 ref NP_038476.2      | bromodomain adjacent to zinc f...    | 55 | 4e-07 | G |
| gi 26338768 dbj BAC33055.1       | unnamed protein product [Mus mu...   | 55 | 4e-07 | G |
| gi 34881239 ref XP_228551.2      | similar to CCG1 [Rattus norveg...    | 55 | 4e-07 | G |
| gi 57090081 ref XP_537409.1      | PREDICTED: similar to bromodom...    | 55 | 4e-07 |   |
| gi 6683494 dbj BAA89209.1        | bromodomain adjacent to zinc fin...  | 55 | 4e-07 | G |
| gi 24659555 ref NP_729188.1      | CG32394-PA [Drosophila melanog...    | 55 | 4e-07 | G |
| gi 32967605 ref NP_872589.1      | bromodomain adjacent to zinc f...    | 55 | 4e-07 | G |
| gi 28958186 gb AAH47418.1        | B430306D02Rik protein [Mus muscu...  | 55 | 4e-07 | G |
| gi 51772243 ref XP_194622.4      | similar to CCG1 [Mus musculus]       | 55 | 4e-07 | G |
| gi 51767276 ref XP_484142.1      | hypothetical protein B930060C0...    | 55 | 4e-07 | G |
| gi 4884108 emb CAB43261.1        | hypothetical protein [Homo sapie...  | 55 | 4e-07 | G |
| gi 40787763 gb AAH65123.1        | BC065123 protein [Mus musculus]      | 55 | 4e-07 | G |
| gi 22653665 sp Q9NRL2 BA1A HUMAN | Bromodomain adjacent to zi...        | 55 | 4e-07 | G |
| gi 26338285 dbj BAC32828.1       | unnamed protein product [Mus mu...   | 55 | 4e-07 | G |
| gi 19075972 ref NP_588472.1      | putative transcriptional regul...    | 55 | 5e-07 | G |
| gi 42549961 gb EAA72804.1        | hypothetical protein FG04423.1 [...  | 55 | 5e-07 | G |
| gi 24020884 gb AAN40840.1        | TBP-associated factor RNA polyme...  | 55 | 5e-07 | G |
| gi 50760409 ref XP_418009.1      | PREDICTED: similar to Transcri...    | 55 | 5e-07 | G |
| gi 50745680 ref XP_420198.1      | PREDICTED: similar to CCG1 [Ga...    | 55 | 5e-07 | G |
| gi 42558222 dbj BAD11104.1       | SNF2-family ATP dependent chrom...   | 55 | 5e-07 |   |
| gi 47209254 emb CAF91993.1       | unnamed protein product [Tetrao...   | 55 | 5e-07 |   |
| gi 56202868 emb CAI21897.1       | tripartite motif-containing 33 ...   | 55 | 7e-07 |   |
| gi 20129741 ref NP_610266.1      | CG1845-PA [Drosophila melanoga...    | 55 | 7e-07 | G |
| gi 34876969 ref XP_240329.2      | similar to polybromo-1D [Rattu...    | 55 | 7e-07 | G |
| gi 57098727 ref XP_533013.1      | PREDICTED: similar to Transcri...    | 55 | 7e-07 |   |
| gi 30721853 gb AAP34197.1        | polybromo-1D [Homo sapiens]          | 55 | 7e-07 | G |
| gi 14971411 ref NP_148980.1      | tripartite motif-containing 33...    | 55 | 7e-07 | G |
| gi 12083896 gb AAG48941.1        | polybromo-1 [Homo sapiens] >gi 4...  | 55 | 7e-07 | G |
| gi 12083894 gb AAG48940.1        | polybromo-1 [Homo sapiens] >gi 4...  | 55 | 7e-07 | G |
| gi 12083892 gb AAG48939.1        | polybromo-1 [Homo sapiens] >gi 3...  | 55 | 7e-07 | G |
| gi 12083875 gb AAG48933.1        | polybromo-1 [Homo sapiens]           | 55 | 7e-07 | G |
| gi 54635374 gb EAL24777.1        | GA14940-PA [Drosophila pseudoobs...  | 55 | 7e-07 |   |
| gi 51768295 ref XP_484357.1      | RIKEN 2310032M22 [Mus musculus]      | 55 | 7e-07 | G |
| gi 46097809 gb EAK83042.1        | hypothetical protein UM05168.1 [...  | 55 | 7e-07 |   |
| gi 30794368 ref NP_060783.2      | polybromo 1 [Homo sapiens] >gi...    | 55 | 7e-07 | G |
| gi 16551971 dbj BAB71210.1       | unnamed protein product [Homo s...   | 55 | 7e-07 | G |


|                                  |                                      |    |       |   |
|----------------------------------|--------------------------------------|----|-------|---|
| gi 4325109 gb AAD17259.1         | transcriptional intermediary fact... | 55 | 7e-07 | G |
| gi 27803071 emb CAD60774.1       | unnamed protein product [Podosp...   | 55 | 7e-07 |   |
| gi 26326785 dbj EAC27136.1       | unnamed protein product [Mus mu...   | 55 | 7e-07 | G |
| gi 26365296 dbj BAB26374.2       | unnamed protein product [Mus mu...   | 55 | 7e-07 | G |
| gi 6755993 ref NP_035844.1       | bromodomain adjacent to zinc fi...   | 54 | 9e-07 | G |
| gi 50417257 gb AAH78299.1        | Zgc:100857 protein [Danio rerio]     | 54 | 9e-07 | G |
| gi 26332264 dbj BAC29862.1       | unnamed protein product [Mus mu...   | 54 | 9e-07 | G |
| gi 56202867 emb CAI21896.1       | tripartite motif-containing 33 ...   | 54 | 1e-06 |   |
| gi 32421217 ref XP_331052.1      | hypothetical protein [Neurospo...    | 54 | 1e-06 | G |
| gi 55620429 ref XP_516515.1      | PREDICTED: similar to polybrom...    | 54 | 1e-06 |   |
| gi 55587792 ref XP_513668.1      | PREDICTED: tripartite motif-co...    | 54 | 1e-06 |   |
| gi 14971413 ref NP_056990.2      | tripartite motif-containing 33...    | 54 | 1e-06 | G |
| gi 56202866 emb CAI21895.1       | tripartite motif-containing 33 ...   | 54 | 1e-06 |   |
| gi 5834582 emb CAB55313.1        | rfg7 protein [Homo sapiens]          | 54 | 1e-06 | G |
| gi 5689563 dbj BAA03065.1        | KIAA1113 protein [Homo sapiens]      | 54 | 1e-06 | G |
| gi 45384026 ref NP_990496.1      | polybromo 1 protein [Gallus ga...    | 54 | 1e-06 | G |
| gi 38197516 gb AAH08965.2        | BAZ2A protein [Homo sapiens]         | 54 | 1e-06 | G |
| gi 57092555 ref XP_538237.1      | PREDICTED: similar to hypothet...    | 54 | 1e-06 |   |
| gi 37194693 gb AAH58241.1        | Unknown (protein for IMAGE:63083...  | 54 | 1e-06 |   |
| gi 7304921 ref NP_038477.1       | bromodomain adjacent to zinc fi...   | 54 | 1e-06 | G |
| gi 14670390 ref NP_075381.2      | bromodomain adjacent to zinc f...    | 54 | 1e-06 | G |
| gi 54648598 gb AAH84946.1        | Unknown (protein for IMAGE:49603...  | 54 | 1e-06 |   |
| gi 33469025 ref NP_473419.1      | bromodomain adjacent to zinc f...    | 54 | 1e-06 | G |
| gi 37360250 dbj BAC98103.1       | mKIAA1113 protein [Mus musculus]     | 54 | 1e-06 | G |
| gi 46229766 gb EAK90584.1        | protein with 2 bromo domains [Cr...  | 54 | 1e-06 |   |
| gi 54657810 gb EAL36527.1        | hypothetical protein Chro.70137 ...  | 54 | 1e-06 |   |
| gi 51476484 emb CAH18232.1       | hypothetical protein [Homo sapi...   | 54 | 1e-06 |   |
| gi 28972143 dbj BAC65525.1       | mKIAA0314 protein [Mus musculus]     | 54 | 1e-06 | G |
| gi 4049922 gb AAC97879.1         | transcription factor WSTF [Homo s... | 54 | 1e-06 | G |
| gi 56490889 emb CAI05770.1       | hypothetical protein PB301534.0...   | 54 | 1e-06 |   |
| gi 22653669 sp Q9UIF9 BA2A_HUMAN | Bromodomain adjacent to zi...        | 54 | 1e-06 | G |
| gi 2224569 dbj BAA20773.1        | KIAA0314 [Homo sapiens]              | 54 | 1e-06 | G |
| gi 474971 dbj BAA05110.1         | CCG1 [Mesocricetus auratus] >gi 2... | 53 | 2e-06 |   |
| gi 34867725 ref XP_221627.2      | similar to WDR9 protein, form ...    | 53 | 2e-06 | G |
| gi 34862191 ref XP_222315.2      | similar to TTF-I interacting p...    | 53 | 2e-06 | G |
| gi 57108950 ref XP_544889.1      | PREDICTED: similar to WD-repea...    | 53 | 2e-06 |   |
| gi 55643327 ref XP_523285.1      | PREDICTED: similar to CREB-bin...    | 53 | 2e-06 |   |
| gi 37360534 dbj BAC98245.1       | mKIAA1740 protein [Mus musculus]     | 53 | 2e-06 | G |
| gi 57229792 gb AAW46194.1        | nucleus protein, putative [Crypt...  | 53 | 3e-06 |   |
| gi 23508824 ref NP_701492.1      | bromodomain protein, putative ...    | 53 | 3e-06 | G |
| gi 45433503 ref NP_444400.1      | tripartite motif protein 33 [M...    | 53 | 3e-06 | G |
| gi 50255361 gb EAL18096.1        | hypothetical protein CNBK1170 [C...  | 53 | 3e-06 |   |
| gi 54637438 gb EAL26840.1        | GA10956-PA [Drosophila pseudoobs...  | 53 | 3e-06 |   |
| gi 51770163 ref XP_196171.4      | bromodomain and PHD finger con...    | 53 | 3e-06 | G |
| gi 55962792 emb CAI11773.1       | novel protein [Danio rerio]          | 53 | 3e-06 |   |
| gi 37360308 dbj BAC98132.1       | mKIAA1286 protein [Mus musculus]     | 53 | 3e-06 | G |
| gi 56518079 emb CAH79038.1       | bromodomain protein, putative [...]  | 53 | 3e-06 |   |
| gi 56515560 emb CAH84003.1       | hypothetical protein PC300805.0...   | 53 | 3e-06 |   |
| gi 23480253 gb EAA16864.1        | ERYTHROCYTE MEMBRANE PROTEIN PFE...  | 53 | 3e-06 |   |

## Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|15706263|emb|CAC69989.1|  bromodomain containing 2 [Homo sapiens]  
Length = 801

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)






Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE  
Sbjct: 81 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 140

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
Sbjct: 141 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 181

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 368 YAWPFYKPVDSALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFNSCYK 427

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 428 YNPPDHDVVAMARKLQDVFEFRYAKMP 454

☐ >gi|4826806|ref|NP\_005095.1|  bromodomain containing protein 2 [Homo sapiens]  
gi|56207529|emb|CAI18689.1| bromodomain containing 2 [Homo sapiens]  
gi|56206429|emb|CAI18548.1| bromodomain containing 2 [Homo sapiens]  
gi|55961972|emb|CAI18110.1| bromodomain containing 2 [Homo sapiens]  
gi|55961413|emb|CAI17492.1| bromodomain containing 2 [Homo sapiens]  
gi|2980663|emb|CAA43996.1|  FSH [Homo sapiens]  
gi|52545950|emb|CAH56171.1|  hypothetical protein [Homo sapiens]  
gi|577293|dbj|BAA07641.1|  KIAA9001 [Homo sapiens]  
gi|12230989|sp|P25440|BRD2 HUMAN  Bromodomain-containing protein 2 (RING3 protei  
Length = 801

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)


Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE  
Sbjct: 81 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 140

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
Sbjct: 141 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 181

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 368 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCKY 427

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 428 YNPPDHDVVAMARKLQDVFEFRIYAKMP 454

>[gi|1082363|pir||A56619](#) female sterile homeotic (fsh) homolog RING3 - human  
[gi|182769|gb|AAA68890.1|](#)  putative  
Length = 754

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)




Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE  
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 321 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCKY 380

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 381 YNPPDHDVVAMARKLQDVFEFRIYAKMP 407

>[gi|51770504|ref|XP\\_489783.1|](#)  similar to MMRING3.1.2 [Mus musculus]  
[gi|3811391|gb|AAC69907.1|](#)  RING3 [Mus musculus]  
[gi|2995270|emb|CAA15819.1|](#) MMRING3.1.2-[Mus musculus]  
[gi|3041763|dbj|BAA25416.1|](#)  Ring3 [Mus musculus]  
Length = 798

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE  
Sbjct: 80 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 139

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101

CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP

Sbjct: 140 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 180

Score = 100 bits (248), Expect = 1e-20

Identities = 46/87 (52%), Positives = 58/87 (66%)


Query: 15 FAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
 +AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY

Sbjct: 367 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 426

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101

YN P D+V MA+ L+ +F + A MP

Sbjct: 427 YNPPDHDVVAMARKLQDVFEFRYAKMP 453

 >gi|57094404|ref|XP\_532103.1| PREDICTED: similar to Bromodomain-containing prote  
 protein) (O27.1.1) [Canis familiaris]  
 Length = 800

Score = 217 bits (553), Expect = 6e-56

Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE

Sbjct: 99 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 158

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP

Sbjct: 159 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 199

Score = 100 bits (248), Expect = 1e-20

Identities = 46/87 (52%), Positives = 58/87 (66%)




Query: 15 FAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
 +AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY

Sbjct: 365 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 424

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101

YN P D+V MA+ L+ +F + A MP

Sbjct: 425 YNPPDHDVVAMARKLQDVFEFRYAKMP 451

 >gi|47059183|ref|NP\_997660.1|  bromodomain-containing 2 [Rattus norvegicus]  
 gi|46237556|emb|CAE83937.1|  bromodomain-containing 2 [Rattus norvegicus]  
 Length = 798

Score = 217 bits (553), Expect = 6e-56

Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE




Sbjct: 80 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 139

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
Sbjct: 140 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 180

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 367 YAWPFYKPVDA SALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 426

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 427 YNPPDHDVVAMARKLQDVFEFRYAKMP 453

 >gi|6753910|ref|NP\_034368.1|  bromodomain containing 2 [Mus musculus]  
gi|3273701|gb|AAC24810.1|  female sterile homeotic-related protein Frg-1 [Mus mu]  
Length = 798

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)


Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE  
Sbjct: 80 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 139

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
Sbjct: 140 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 180

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 367 YAWPFYKPVDA SALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 426

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 427 YNPPDHDVVAMARKLQDVFEFRYAKMP 453

 >gi|55956582|emb|CAI11405.1| bromodomain-containing protein 2 [Canis familiaris]  
Length = 803

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE  
Sbjct: 81 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 140



Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
 Sbjct: 141 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 181

Score = 100 bits (248), Expect = 1e-20  
 Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
 +AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
 Sbjct: 368 YAWPFYKPVDA SALGLHDYHDI IKHPMDLSTV KRKMENRDYRDAQEFAADVRLMFSNCYK 427

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
 YN P D+V MA+ L+ +F + A MP  
 Sbjct: 428 YNPPDHDVVAMARKLQDVFEFRYAKMP 454

>gi|55725298|emb|CAH89514.1| hypothetical protein [Pongo pygmaeus]  
 Length = 546

Score = 217 bits (553), Expect = 6e-56  
 Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60  
 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE  
 Sbjct: 81 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 140

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
 Sbjct: 141 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 181

Score = 100 bits (248), Expect = 1e-20  
 Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
 +AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
 Sbjct: 368 YAWPFYKPVDA SALGLHDYHDI IKHPMDLSTV KRKMENRDYRDAQEFAADVRLMFSNCYK 427

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
 YN P D+V MA+ L+ +F + A MP  
 Sbjct: 428 YNPPDHDVVAMARKLQDVFEFRYAKMP 454

>gi|52545923|emb|CAH56179.1| hypothetical protein [Homo sapiens]  
 Length = 754

Score = 217 bits (553), Expect = 6e-56  
 Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60  
 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE  
 Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 93



Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101

CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 321 YAWPFYKPVDA SALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 380

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 381 YNPPDHDVVAMARKLQDVFEFRYAKMP 407

 >gi|12802529|gb|AAK07919.1|  ring 3 [Mus musculus]  
Length = 503

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)



Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE  
Sbjct: 80 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 139

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
Sbjct: 140 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 180

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 367 YAWPFYKPVDA SALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 426

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 427 YNPPDHDVVAMARKLQDVFEFRYAKMP 453

 >gi|1370115|emb|CAA65450.1|  kinase [Homo sapiens]  
Length = 754

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE  
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP

Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 321 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 380

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 381 YNPPDHDVVAMARKLQDVFEFRYAKMP 407

 >gi|2995269|emb|CAA15818.1|  MMRING3.1.1 [Mus musculus]  
Length = 752

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)




Query: 1 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE  
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 321 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 380

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 381 YNPPDHDVVAMARKLQDVFEFRYAKMP 407

 >gi|2780779|dbj|BAA24379.1|  Ring3 [Mus musculus]  
gi|2780777|dbj|BAA24378.1|  Ring3 [Mus musculus]  
Length = 503

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE  
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 93



Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP

Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 321 YAWPFYKPVDA SALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 380

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 381 YNPPDHDVVAMARKLQDVFEFRYAKMP 407

 >gi|2780775|dbj|BAA24377.1|  Ring3 [Mus musculus]  
Length = 549

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE  
Sbjct: 80 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 139

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
Sbjct: 140 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 180

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 367 YAWPFYKPVDA SALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 426

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 427 YNPPDHDVVAMARKLQDVFEFRYAKMP 453

 >gi|39645317|gb|AAH63840.1|  BRD2 protein [Homo sapiens]  
Length = 836

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE  
Sbjct: 81 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 140

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
Sbjct: 141 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 181

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 368 YAWPFYKPVDASALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNICY 427

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 428 YNPPDHDVVAMARKLQDVFEFRYAKMP 454

>gi|1588281|prf|2208296A RING3 protein  
Length = 509

Score = 217 bits (553), Expect = 6e-56  
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE  
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP  
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20  
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY  
Sbjct: 203 YAWPFYKPVDASALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNICY 262

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F + A MP  
Sbjct: 263 YNPPDHDVVAMARKLQDVFEFRYAKMP 289

>gi|1370092|emb|CAA65449.1| kinase [Gallus gallus]  
Length = 729

Score = 213 bits (542), Expect = 1e-54  
Identities = 98/101 (97%), Positives = 99/101 (98%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYW A+E  
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWGAAE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVA MP  
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVAQMP 134

Score = 100 bits (250), Expect = 8e-21  
Identities = 47/87 (54%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH+IIK PMD+ TIKR++EN Y A E D MF+NCY  
Sbjct: 315 YAWPFYKPVDASALGLHDYHEIIKHPMDLSTIKRK MENRDYHDAQEFAADVRLMFSN CYK 374

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F A MP  
Sbjct: 375 YNPPDHDVVAMARKLQDVFEFSYAKMP 401

>gi|3129967|emb|CAA18965.1| RING3 kinase [synthetic construct]  
gi|7512236|pir||T28145 RING3 kinase - chicken  
Length = 733

Score = 213 bits (542), Expect = 1e-54  
Identities = 98/101 (97%), Positives = 99/101 (98%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYW A+E  
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWGAAE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVA MP  
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVAQMP 134

Score = 100 bits (250), Expect = 8e-21  
Identities = 47/87 (54%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74  
+AWPF +PVDA LGL DYH+IIK PMD+ TIKR++EN Y A E D MF+NCY  
Sbjct: 319 YAWPFYKPVDASALGLHDYHEIIKHPMDLSTIKRK MENRDYHDAQEFAADVRLMFSN CYK 378

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101  
YN P D+V MA+ L+ +F A MP  
Sbjct: 379 YNPPDHDVVAMARKLQDVFEFSYAKMP 405

>gi|34392374|dbj|BAC82511.1| Serine threonine Kinase [Coturnix japonica]  
Length = 735

Score = 213 bits (542), Expect = 1e-54  
Identities = 98/101 (97%), Positives = 99/101 (98%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60  
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYW A+E  
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWGAAE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101  
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVA MP  
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVAQMP 134